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NTDB id 1169 A1552VC RS11075 WP 000648511.1
NTDB id 973176 WMZ02 RS13340 WP 005479682.1
NTDB id 1402 DSB67 RS12670 WP 010643257.1
NTDB id 1112 NCFG RS09215 WP 003689811.1
NTDB id 1113 AAA85695.1 219..1451( )
NTDB id 1252 GC085 RS07730 WP 011213805.1
NTDB id 1198 PSJM300 03950 AFN76868.1
NTDB id 1016 ACIAD RS01680 WP 004920476.1
NTDB id 1059 ABD1 RS01610 WP 000279215.1
consensus

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logo

EIR	DVA	G	M	A	M	R	N	T	N	F	P	N	M	L	Q	N	V	A	G	E	E	S	G	D	D	M	L	N	K	V	A	T	I	Y	E	F	E	V	D	N	V	D	L	S	S	M	E	P	L	I	V	L	G	Y	W	G	G	L																						
KV	Y	E	T	S	G	Q	P	L	S	S	E	X	C	E	K	F	L	M	A	T	S	A	R	E	E	S	D	I	A	T	E	Y	F	D	N	K	V	A	T	I	Y	E	F	E	V	D	N	V	D	L	S	S	M	E	P	L	I	V	L	G	Y	W	G	G	L															
E	V	Y	R	D	T	A	A	G	M	P	M	Y	I	A	M	R	N	C	N	V	F	P	E	L	V	L	Q	M	V	M	I	G	E	E	S	G	Q	L	D	D	M	L	N	K	V	A	T	I	Y	E	F	E	V	D	N	V	D	N	L	G	K	T	I	L	E	P	L	I	I	V	F	L	G	T	V	V	G	G	L	
E	V	Y	R	D	T	A	A	G	M	P	M	Y	I	A	M	R	N	C	N	V	F	P	E	L	V	L	Q	M	V	M	I	G	E	E	S	G	R	L	D	D	M	L	N	K	V	A	T	I	Y	E	F	E	V	D	N	V	D	N	L	S	K	I	L	E	P	L	I	I	V	F	L	G	T	V	V	G	G	L		
E	V	Y	R	D	T	A	A	G	M	P	M	Y	I	A	M	R	H	C	H	V	F	P	E	L	V	L	Q	M	V	M	I	G	E	E	S	G	R	L	D	D	M	L	N	K	V	A	T	I	Y	E	F	E	V	D	N	V	D	N	L	S	K	I	L	E	P	L	I	I	V	F	L	G	T	V	V	G	G	L		
E	I	R	T	R	V	I	Q	G	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	S	S	I	G	E	E	S	G	S	L	D	D	M	L	N	K	A	A	E	F	Y	E	D	E	V	D	N	A	V	G	R	L	S	A	M	M	E	P	I	I	I	V	L	G	L	V	I	G	T	L			
E	I	R	T	R	V	I	Q	G	L	S	M	T	S	G	M	R	A	T	E	L	F	P	N	M	L	Q	M	S	S	I	G	E	E	S	G	S	L	D	D	M	L	N	K	A	A	E	F	Y	E	D	E	V	D	N	A	V	G	R	L	S	A	M	M	E	P	I	I	I	L	G	L	V	I	G	T	L				
K	I	R	E	V	A	T	G	Q	Q	M	F	I	A	M	E	N	T	H	L	F	P	N	M	I	Q	M	V	A	I	G	E	E	S	G	A	L	E	K	M	L	S	K	V	A	D	E	F	Y	E	E	V	N	N	A	V	D	A	L	S	S	L	E	P	I	I	M	S	I	L	G	I	L	V	G	G	L				
K	I	K	S	D	V	S	S	G	M	Q	L	N	F	S	M	R	T	V	G	R	F	P	S	M	A	V	Q	M	T	A	I	G	E	E	S	G	A	L	D	E	M	L	S	K	V	A	T	E	F	Y	E	D	E	V	D	N	M	V	D	G	L	T	A	L	M	E	P	M	I	M	A	V	L	G	V	L	V	G	G	L
K	I	R	E	D	V	T	G	Q	Q	L	N	F	A	M	R	T	S	N	R	F	P	S	M	A	I	Q	M	V	A	I	G	E	E	S	G	A	L	D	E	M	L	S	K	V	A	T	E	F	Y	E	D	E	V	D	N	M	V	D	G	L	T	S	M	M	E	P	L	I	M	A	I	L	G	I	L	V	G	G	L	
K	I	R	E	D	V	A	T	G	Q	Q	L	N	F	A	M	R	I	S	N	R	F	P	S	M	A	I	Q	M	V	A	I	G	E	E	S																																													

Position	1	2	3	4	5	6	7	8	9	10
Sequence	VV	AM	YL	PI	FN	LG	SW	GA		
408	V	A	M	Y	L	P	I	F	N	L
407	V	T	A	M	Y	L	P	I	F	N
407	V	T	A	M	Y	L	P	I	F	N
410	L	V	A	M	Y	L	P	I	F	N
410	L	V	A	M	Y	L	P	I	F	N
406	I	I	A	M	Y	L	P	I	F	N
405	V	I	A	M	Y	L	P	I	F	N
408	V	I	A	M	Y	L	P	I	F	N
408	V	I	A	M	Y	L	P	I	F	N

* * * * * * * * * *

- non conserved
- similar
- $\geq 50\%$ conserved